

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 08/444791
Source: IFW16
Date Processed by STIC: 12/20/04

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/20/2004

PATENT APPLICATION: US/08/444,791

TIME: 13:10:36

Input Set : A:\40451C.txt

Output Set: N:\CRF4\12202004\H444791.raw

3 <110> APPLICANT: Brockhaus, et al.
 5 <120> TITLE OF INVENTION: Human TNF Receptor
 7 <130> FILE REFERENCE: 01017/40451C
 9 <140> CURRENT APPLICATION NUMBER: US 08/444,791
 10 <141> CURRENT FILING DATE: 1995-05-19
 12 <150> PRIOR APPLICATION NUMBER: CH 3319/89
 13 <151> PRIOR FILING DATE: 1989-09-12
 15 <150> PRIOR APPLICATION NUMBER: CH 786/90
 16 <151> PRIOR FILING DATE: 1990-03-08
 18 <150> PRIOR APPLICATION NUMBER: CH 1347/90
 19 <151> PRIOR FILING DATE: 1990-04-20
 21 <150> PRIOR APPLICATION NUMBER: US 07/580,013
 22 <151> PRIOR FILING DATE: 1990-09-10
 24 <150> PRIOR APPLICATION NUMBER: US 08/095,640
 25 <151> PRIOR FILING DATE: 1993-07-21
 27 <160> NUMBER OF SEQ ID NOS: 26
 29 <170> SOFTWARE: PatentIn version 3.3
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 2111
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Homo sapiens
 36 <400> SEQUENCE: 1

37	gaattcgggg	gggttcaaga	tacttggggac	caggccgtga	tctctatgcc	cgagtctcaa	60
39	ccctcaactg	tcaccccaag	gcacttggga	cgctcctggac	agaccgagtc	ccgggaagcc	120
41	ccagcactgc	cgctgccaca	ctgccctgag	cccaaatggg	ggagtgagag	gccatagctg	180
43	tctggcatgg	gcctctccac	cgtgcctgac	ctgctgctgc	cgctggtgct	cctggagctg	240
45	ttggtgggaa	tatacccctc	aggggttatt	ggactgggtcc	ctcacctagg	ggacagggag	300
47	aagagagata	gtgtgtgtcc	ccaaggaaaa	tatatccacc	ctcaaaataa	ttcgatttgc	360
49	tgtaccaagt	gccacaaagg	aacctacttg	tacaatgact	gtccaggccc	ggggcaggat	420
51	acggactgca	gggagtgtga	gagcggctcc	ttcaccgctt	cagaaaacca	cctcagacac	480
53	tgcctcagct	gctccaaatg	ccgaaaggaa	atgggtcagg	tggagatctc	ttcttgcaca	540
55	gtggaccggg	acaccgtgtg	tggctgcagg	aagaaccagt	accggcatta	ttggagtga	600
57	aaccttttcc	agtgttcaa	ttgcagcctc	tgcttcaatg	ggaccgtgca	cctctcctgc	660
59	caggagaaac	agaacaccgt	gtgcacctgc	catgcagggt	tcttttctaag	agaaaacgag	720
61	tgtgtctcct	gtagtaactg	taagaaaagc	ctggagtgc	cgaagtgtgt	cctaccccag	780
63	attgagaatg	ttaagggcac	tgaggactca	ggcaccacag	tgctgttgcc	cctggtcatt	840
65	ttcttttggtc	tttgccctttt	atccctcctc	ttcattgggt	taatgtatcg	ctaccaacgg	900
67	tggaaagtcca	agctctactc	cattgtttgt	gggaaatcga	cacctgaaaa	agagggggag	960
69	cttgaaggaa	ctactactaa	gcccctggcc	ccaaacccaa	gcttcagtcc	cactccaggc	1020
71	ttcacccccca	ccctgggctt	cagtcctgtg	cccagttcca	ccttcacctc	cagctccacc	1080
73	tatacccccg	gtgactgtcc	caactttgcg	gctccccgca	gagaggtggc	accaccctat	1140
75	cagggggctg	accccatcct	tgcgacagcc	ctgcctcctg	accccatccc	caacccctt	1200
77	cagaagtggg	aggacagcgc	ccacaagcca	cagagcctag	acactgatga	ccccgcgacg	1260

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79 ctgtacgcgcg tgggtggagaa cgtgcccccg ttgcgctgga aggaattcgt gcggcgcccta 1320
81 gggctgagcg accacgagat cgatcggtcg gagctgcaga acgggcgctg cctgcgcgag 1380
83 gcgcaataca gcatgctggc gacctggagg cggcgacgc cgcggcgcga ggccacgctg 1440
85 gagctgctgg gaogcgtgct cgcgcacatg gacctgctgg gctgcctgga ggacatcgag 1500
87 gaggcgcttt gcggccccgc cgcctccccg cccgcgcccc gtcttctcag atgaggctgc 1560
89 gccccctgcgg gcagctctaa ggaccgtcct gcgagatcgc ctccaaccc cacttttttc 1620
91 tggaaaggag gggctcctgca ggggcaagca ggagctagca gccgcctact tgggtgctaac 1680
93 cctcgatgt acatagcttt tctcagctgc ctgcgcgcgc cgcacagtca gcgctgtgcg 1740
95 cgcggagaga ggtgcgcgt gggctcaaga gcctgagtgg gtggtttgcg aggatgaggg 1800
97 acgctatgcc tcatgccgt tttgggtgtc ctcaccagca aggctgctcg ggggccctg 1860
99 gttcgtccct gaggcttttt cacagtgcac aagcagtttt ttttgttttt gtttggtttt 1920
101 gttttgtttt taaatcaatc atgttacact aatagaaact tggcactcct gtgccctctg 1980
103 cctggacaag cacatagcaa gctgaactgt cctaaggcag gggcgagcac ggaacaatgg 2040
105 ggccttcagc tggagctgtg gacttttgta catacactaa aattctgaag ttaaaaaaaaa 2100
107 aacccgaatt c 2111
110 <210> SEQ ID NO: 2
111 <211> LENGTH: 455
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 2
117 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
118 1 5 10 15
121 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
122 20 25 30
125 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
126 35 40 45
129 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
130 50 55 60
133 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
134 65 70 75 80
137 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
138 85 90 95
141 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
142 100 105 110
145 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
146 115 120 125
149 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
150 130 135 140
153 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
154 145 150 155 160
157 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
158 165 170 175
161 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
162 180 185 190
165 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
166 195 200 205
169 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
170 210 215 220
173 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys

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174 225          230          235          240
177 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
178          245          250          255
181 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
182          260          265          270
185 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
186          275          280          285
189 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
190          290          295          300
193 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
194 305          310          315          320
197 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
198          325          330          335
201 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
202          340          345          350
205 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
206          355          360          365
209 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
210          370          375          380
213 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
214 385          390          395          400
217 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
218          405          410          415
221 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
222          420          425          430
225 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
226          435          440          445
229 Pro Ala Pro Ser Leu Leu Arg
230          450          455

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233 <210> SEQ ID NO: 3

234 <211> LENGTH: 2339

235 <212> TYPE: DNA

236 <213> ORGANISM: Homo sapiens

238 <400> SEQUENCE: 3

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239 tcggacaccg tgtgtgactc ctgtgaggac agcacataca cccagctctg gaactggggtt      60
241 cccgagtgtc tgagctgtgg ctcccgtgtg agctctgacc aggtggaaac tcaagcctgc      120
243 actcgggaac agaaccgcat ctgcacctgc aggcccggct ggtactgctc gctgagcaag      180
245 caggaggggt gccggctgtg cgcgccgtg ccgaagtgcc gcccgggctt cggcgtggcc      240
247 agaccaggaa ctgaaacatc agacgtggtg tgcaagccct gtgccccggg gacgttctcc      300
249 aacacgactt catccacgga tatttgcagg ccccaccaga tctgtaacgt ggtggccatc      360
251 cctgggaatg caagcaggga tgcagtctgc acgtccacgt ccccccaccg gagtatggcc      420
253 ccaggggcag tacacttacc ccagccagtg tccacacgat cccaacacac gcagccaagt      480
255 ccagaaccca gcaactgctcc aagcacctcc ttctgtctcc caatgggccc cagcccccca      540
257 gctgaaggga gcactggcga cttcgctctt ccagttggac tgattgtggg tgtgacagcc      600
259 ttgggtctac taataatagg agtggtgaac tgtgtcatca tgaccaggt gaaaaagaag      660
261 cccttgtgcc tgcagagaga agccaagggt cctcacttgc ctgccgataa ggccccgggt      720
263 acacagggcc ccgagcagca gcacctgtg atcacagcgc cgagctccag cagcagctcc      780
265 ctggagagct cggccagtgc gttggacaga agggcgccca ctcggaacca gccacaggca      840
267 ccaggcgtgg aggccagtgg ggccggggag gcccgggcca gcaccgggag ctcagcagat      900

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269 tcttccccctg gtggccatgg gacccaggtc aatgtcacct gcatcgtgaa cgtctgtagc 960
271 agctctgacc acagctcaca gtgtcctccc caagccagct ccacaatggg agacacagat 1020
273 tccagccccc cggagtcccc gaaggacgag caggtccccc tctccaagga ggaatgtgcc 1080
275 tttcgggtcac agctggagac gccagagacc ctgctgggga gcaccgaaga gaagcccctg 1140
277 ccccttgtag tgccctgatgc tgggatgaag cccagttaac caggccggtg tgggctgtgt 1200
279 cgtagccaag gtggctgagc cctggcagga tgaccctgcg aaggggccct ggtccttcca 1260
281 ggccccccacc actaggactc tgaggctctt tctgggccaa gttcctctag tgccctccac 1320
283 agccgcagcc tccctctgac ctgcaggcca agagcagagg cagcgagttg tggaaagcct 1380
285 ctgctgccat ggcgtgtccc tctcggaagg ctggctgggc atggacgttc ggggcatgct 1440
287 ggggcaagtc cctgagtctc tgtgacctgc cccgccagc tgcacctgcc agcctggctt 1500
289 ctggagccct tgggtttttt gtttgtttgt ttgtttgttt gtttgtttct cccctgggc 1560
291 tctgccagc tctggcttcc agaaaacccc agcatccttt tctgcagagg ggctttctgg 1620
293 agaggaggga tgctgcctga gtcacccatg aagacaggac agtgcttcag cctgaggctg 1680
295 agactgcggg atggtcctgg ggctctgtgc agggaggagg tggcagccct gtagggaacg 1740
297 gggctccttca agttagctca ggaggcttg aaagcatcac ctgaggccag gtgcagtggc 1800
299 tcacgcctat gatcccagca ctttgggagg ctgaggcggg tggatcacct gaggttagga 1860
301 gttcgagacc agcctggcca acatggtaaa accccatctc tactaaaaat acagaaatta 1920
303 gccgggcgtg gtggcgggca cctatagtcc cagctactca gaagcctgag gctgggaaat 1980
305 cgtttgaacc cgggaagcgg aggttgccagg gagccgagat cagccactg cactccagcc 2040
307 tgggcgacag agcgagagtc tgtctcaaaa gaaaaaaaaa aagcaccgcc tccaaatgct 2100
309 aacttgtcct tttgtaccat ggtgtgaaag tcagatgccc agagggccca ggcaggccac 2160
311 catattcagt gctgtggcct gggcaagata acgcacttct aactagaaat ctgccattt 2220
313 tttaaaaaag taagtaccac tcaggccaac aagccaacga caaagccaa ctctgccagc 2280
315 cacatccaac cccccacctg ccatttgcac cctccgcctt cactccggtg tgccctgcag 2339

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320 <210> SEQ ID NO: 4

321 <211> LENGTH: 392

322 <212> TYPE: PRT

323 <213> ORGANISM: Homo sapiens

325 <400> SEQUENCE: 4

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327 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
328 1 5 10 15
331 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
332 20 25 30
335 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
336 35 40 45
339 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
340 50 55 60
343 Arg Leu Cys Ala Pro Leu Pro Lys Cys Arg Pro Gly Phe Gly Val Ala
344 65 70 75 80
347 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
348 85 90 95
351 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
352 100 105 110
355 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
356 115 120 125
359 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
360 130 135 140
363 His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Ser
364 145 150 155 160

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367 Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
368                               165                               170                               175
371 Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val
372                               180                               185                               190
375 Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val
376                               195                               200                               205
379 Val Asn Cys Val Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu
380                               210                               215                               220
383 Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala Asp Lys Ala Arg Gly
384 225                               230                               235                               240
387 Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser
388                               245                               250                               255
391 Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala
392                               260                               265                               270
395 Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala
396                               275                               280                               285
399 Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Ala Asp Ser Ser Pro Gly
400                               290                               295                               300
403 Gly His Gly Thr Gln Val Asn Val Thr Cys Ile Val Asn Val Cys Ser
404 305                               310                               315                               320
407 Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met
408                               325                               330                               335
411 Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro Lys Asp Glu Gln Val
412                               340                               345                               350
415 Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro
416                               355                               360                               365
419 Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val
420                               370                               375                               380
423 Pro Asp Ala Gly Met Lys Pro Ser
424 385                               390

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427 <210> SEQ ID NO: 5

428 <211> LENGTH: 28

429 <212> TYPE: PRT

430 <213> ORGANISM: Artificial sequence

432 <220> FEATURE:

433 <223> OTHER INFORMATION: Synthetic peptide

435 <220> FEATURE:

436 <221> NAME/KEY: misc_feature

437 <222> LOCATION: (25)..(25)

438 <223> OTHER INFORMATION: Xaa = any or unknown amino acid

440 <400> SEQUENCE: 5

442 Leu Val Pro His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro

443 1 5 10 15

W--> 446 Gln Gly Lys Tyr Ile His Pro Glu Xaa Asn Ser Ile

447 20 25

449 <210> SEQ ID NO: 6

450 <211> LENGTH: 15

451 <212> TYPE: PRT

452 <213> ORGANISM: Artificial sequence

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 25

Seq#:10; Xaa Pos. 8

Seq#:11; Xaa Pos. 2

Seq#:14; Xaa Pos. 9,10,13

VERIFICATION SUMMARY

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L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:16
L:526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0